



SEQUENCE LISTING

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HANSEN, Hans

<120> IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
LYMPHOMA AND LEUKEMIA CELLS

<130> 018733/0996

<140> US 09/741,843

<141> 2000-12-22

<150> US 09/127,902

<151> 1998-08-03

<150> US 08/690,102

<151> 1996-07-06

<150> US 08/289,576

<151> 1994-08-12

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 339

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(339)

<223>

<400> 1

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gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
85 90 95

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336
Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

cgt
Arg

339

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<212> PRT
<213> Murinae gen. sp.

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Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 3
<211> 348
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<213> Murinae gen. sp.

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<221> CDS
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Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys Pro Gly Ala
1 5 10 15

48

tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

96

tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att
Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

144

45

35					40					45						
gga	tac	att	aat	cct	agg	aat	gat	tat	act	gag	tac	aat	cag	aac	ttc	192
Gly	Tyr	Ile	Asn	Pro	Arg	Asn	Asp	Tyr	Thr	Glu	Tyr	Asn	Gln	Asn	Phe	
50						55					60					
aag	gac	aag	gcc	aca	ttg	act	gca	gac	aaa	tcc	tcc	agc	aca	gcc	tac	240
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
65					70					75					80	
atg	caa	ctg	agc	agc	ctg	aca	tct	gag	gac	tct	gca	gtc	tat	tac	tgt	288
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
gca	aga	agg	gat	att	act	acg	ttc	tac	tgg	ggc	caa	ggc	acc	act	ctc	336
Ala	Arg	Arg	Asp	Ile	Thr	Thr	Phe	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	
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aca	gtc	tcc	tcg													348
Thr	Val	Ser	Ser													
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<210> 4
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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
 100 105 110

Thr Val Ser Ser
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 <212> DNA
 <213> Homo sapiens

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 <222> (1)..(339)
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 gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa 144
 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 35 40 45
 gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc 240
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
 65 70 75 80
 atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa 288
 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
 85 90 95
 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa 336
 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
 100 105 110
 cgt 339
 Arg

<210> 6
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 6
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 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30
 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 35 40 45
 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys
100 105 110

Arg

<210> 7
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(348)
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1 5 10 15

tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att 144
Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac 240
Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt 288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc 336
Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

acc gtc tcc tcg 348
Thr Val Ser Ser
115

<210> 8
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<212> PRT
<213> Homo sapiens

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1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 9
<211> 116
<212> PRT
<213> Homo sapiens

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Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 10
<211> 149
<212> DNA
<213> Unknown

<220>
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tgacccagtg cagccagtag ctagtaaagg tgtagccaga agccttgtag gagacattca 120
ctgatgaccc aggtttcttg acttcagcc 149

<210> 11
<211> 134
<212> DNA
<213> Unknown

<220>
<223> synthetic sequence

<400> 11
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ctgctcagct ccatgtaggc tgtattggtg gattcgtctg cagttattgt ggccttgctc 120
ttgaagttct gatt 134

<210> 12
<211> 38
<212> DNA
<213> Unknown

<220>
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<400> 12
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<210> 13
<211> 33
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 13
aagtggatcc tataatcatt cctaggatta atg 33

<210> 14
<211> 49
<212> DNA
<213> Unknown

<220>
<223> primer

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taatcctagg aatgattata ctgagtacaa tcagaacttc aaggacaag

49

<210> 15
<211> 44
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 15
ggagacggtg accgtggtgc cttggcccca gtagaacgta gtaa

44

<210> 16
<211> 150
<212> DNA
<213> Unknown

<220>
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ggccaagtag ttcttgtgat ttgcactgta taaaacactt tgactggact tacagctcat 120
agtgacccta tctccaacag atgcgctcag 150

<210> 17
<211> 52
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 17
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<210> 18
<211> 45
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 18
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<210> 19
<211> 121
<212> DNA
<213> Unknown

<220>
<223> synthetic sequence

<400> 19
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caatgtcttc tggttgaaga gagctgatgg tgaaagtaaa atctgtccca gatccgctgc 120
c 121

<210> 20
<211> 40
<212> DNA
<213> Unknown

<220>
<223> primer

<400> 20
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<210> 21
<211> 33
<212> DNA
<213> Unknown

<220>
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<400> 21
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agatccgctg cctgtgaagc gatcaggggac accagattcc ctagtggatg cccagtagat 180
cagcagttta ggagactgcc ctggtttctg ctggtaccag gccaaagtagt tcttgtgatt 240
tgcactgtat aaaacacttt gactggactt acagctcata gtgacgtttt ctcttcgaga 300
cacagccaga gatgatggag actgggtcag ctgaatgtc 339

<210> 23
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<212> DNA
<213> Murinae gen. sp.

<220>
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<222> (1) .. (348)
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ggaggatttg tctgcagtca atgtggcctt gtccttgaag ttctgattgt actcagtata 180
atcattccta ggattaatgt atccaatcca ttccagacct tgtccaggcc tctgttttat 240
ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaca tcttcactga 300
ggccccaggt tttgacagtt cagccccctga ctctgcagc tggacctg 348

<210> 24
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(339)
<223>

<400> 24
acgtttgatc tgcaccttgg tccctccacc gaacgtccac gaggagaggt attggtgaca 60
ataatatgtt gcaatgtctt ctggttgaag agagctgatg gtgaaagtaa aatctgtccc 120
agatccgctg ccagagaatc gcgaaggagc accagattcc ctagtggatg cccagtagat 180
cagcagttta ggtgctttcc ctggtttctg ctggtaccag gccaaagtagt tcttgtgatt 240
tgcactgtat aaaacacttt gactggactt acagctcata gtgaccctat ctccaacaga 300
tgcgctcaga gatgatggag actgggtcag ctgaatgtc 339

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<211> 348
<212> DNA
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<220>
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<222> (1)..(348)
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<400> 25
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acaaaaataa aatgccgtgt cctcagacct caggctgctc agctccatgt aggctgtatt 120
ggtggattcg tctgcagtta ttgtggcctt gtccttgaag ttctgattgt actcagtata 180
atcattccta ggattaatgt atccaatcca ttccagacct tgtccagggt cctgcctgac 240
ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaga ccttcactga 300
tgaccaggt ttcttgactt cagccccctga ttggaccagc tggacctg 348